



SEQUENCE LISTING

<110> CHANG, Y-H
VETRO, J.A.
MICKA, W.S.

<120> Dominant Negative Variants of Methionine Aminopeptidase
2 ("MetAP2") and Clinical Uses Therefor

<130> 16153-8007

<140>

<141>

<160> 26

<170> PatentIn Ver. 2.0

<210> 1

<211> 71

<212> PRT

<213> Human polylysine

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Gly Glu Gln Glu Pro Asp Lys Glu Ser Gly Ala Ser Val Asp Glu Val
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Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu Arg Asp Glu
35 40 45

Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Thr Gly Lys Lys
50 55 60

Lys Lys Lys Lys Lys Lys Lys
65 70

<210> 2

<211> 71

<212> PRT

<213> Mouse polylysine

<400> 2

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Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu Arg Asp Asp
35 40 45

Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr Gly Lys Lys
50 55 60

Lys Lys Lys Lys Lys Lys Lys
65 70

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<212> PRT

<213> Saccharomyces polylysine

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 Glu Ser Asp Pro Val Glu Ser Lys Lys Lys Lys Asn Lys Lys Lys Lys
 35 40 45
 Lys Lys Lys Ser Asn Val Lys Lys Ile
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 <212> DNA
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 <213> Artificial Sequence

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 Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Ser Lys Gly Pro
 35 40 45
 Ser Ala Ala Gly Glu Gln Glu Pro Asp Lys Glu Ser Gly Ala Ser Val
 50 55 60
 Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu
 65 70 75 80
 Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Gln Tyr
 325 330 335
 Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
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 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Leu
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<212> PRT

<213> Mouse MetAP2

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 Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
 35 40 45
 Val Ser Ala Val Gln Gln Glu Leu Asp Lys Glu Ser Gly Ala Leu Val
 50 55 60
 Asp Glu Val Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu
 65 70 75 80

Arg Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr
 325 330 335
 Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430

Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
 435 440 445

Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Leu
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Arg Pro Thr Cys Lys Glu Val Val Ser Arg Gly Asp Asp Tyr
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Asp Glu Ser Asp Pro Val Glu Ser Lys Lys Lys Lys Asn Lys Lys Lys
 35           40           45

Lys Lys Lys Lys Ser Asn Val Lys Lys Ile Glu Leu Leu Phe Pro Asp
 50           55           60

Gly Lys Tyr Pro Glu Gly Ala Trp Met Asp Tyr His Gln Asp Phe Asn
 65           70           75           80

Leu Gln Arg Thr Thr Asp Glu Glu Ser Arg Tyr Leu Lys Arg Asp Leu
 85           90           95

Glu Arg Ala Glu His Trp Asn Asp Val Arg Lys Gly Ala Glu Ile His
100           105           110

Arg Arg Val Arg Arg Ala Ile Lys Asp Arg Ile Val Pro Gly Met Lys
115           120           125

Leu Met Asp Ile Ala Asp Met Ile Glu Asn Thr Thr Arg Lys Tyr Thr
130           135           140

Gly Ala Glu Asn Leu Leu Ala Met Glu Asp Pro Lys Ser Gln Gly Ile
145           150           155           160

Gly Xaa Pro Thr Gly Leu Ser Leu Asn His Cys Ala Ala Xaa Phe Thr
165           170           175

Pro Asn Ala Gly Asp Lys Thr Val Leu Lys Tyr Glu Asp Val Met Lys
180           185           190

Val Xaa Tyr Gly Val Gln Val Asn Gly Asn Ile Ile Xaa Ser Ala Phe
195           200           205

Thr Val Ser Phe Asp Pro Gln Tyr Asp Asn Leu Leu Ala Ala Val Lys
210           215           220

Asp Ala Thr Tyr Thr Gly Ile Lys Glu Ala Gly Ile Asp Val Arg Leu
225           230           235           240

Thr Asp Ile Gly Glu Ala Ile Gln Glu Val Met Glu Ser Tyr Glu Val
245           250           255

Glu Ile Asn Gly Glu Thr Tyr Gln Val Lys Pro Cys Arg Asn Xaa Cys
260           265           270

Gly Xaa Ser Ile Ala Pro Tyr Arg Xaa Xaa Gly Gly Lys Ser Val Pro
275           280           285

Ile Val Lys Asn Gly Asp Thr Thr Lys Met Glu Glu Gly Glu His Phe
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ggagcctcag	tggatgaagt	agcaagacag	ttggaaaagt	cagcattgga	agataaagaa	240
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tgtgacctgt	atcctaattg	tgtatttccc	aaaggacaag	aatgcgaata	cccaccaca	420
caagatggcg	gaacagctgc	ttggagaact	acaagtgaag	aaaagaaagc	attagatcag	480
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gtattactag	atgatgacat	ctgtaaaata	gactttggaa	cacatataag	tgagaggatt	780
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caagtgaaac	caatccgtaa	tctaattgga	cattcaattg	ggcaatatag	aatacatgct	1020
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tatgcaattg	aaaccctttg	tagtacagga	aaaggtgttg	ttcatgatga	tatggaatgt	1140
tcacattaca	tgaaaaattt	tgatgttgga	catgtgccaa	taaggcttcc	aagaacaaaa	1200
cacttggttaa	atgtcatcaa	tgaaaaacttt	ggaacccttg	ccttctgccg	cagatggctg	1260
gatcgctttg	gagaaaagtaa	atacttgatg	gctctgaaga	atctgtgtga	cttgggcatt	1320
gtagatccat	atccaccatt	atgtgacatt	aaaggatcat	atacagcgca	atttgaacat	1380
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gatcgcttgg gagaaagtaa atacttaatg gctctgaaga atctgtgtga cttgggcatt 1320
gtagatccat acccaccact gtgtgacatt aaagggtcat atacagcaca gtttgaacac 1380
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aaaaagaaga agaacaagaa aaagaagaag aagaaaagca atgtgaagaa gattgaatta 180
ctgtttccag atggaaaagta cccagaagggt gcgtggatgg actatcatca agatttcaat 240
ctgcaaagaa ccacggatga agaatcacgt tatttgaaaa gggatctgga aagggccgaa 300
cattggaatg atgtcagaaa ggggtgctgag atacatcgct gtgtgagaag ggccatcaag 360
gacagaatcg ttcctgggat gaagttaatg gatatcgctg acatgatcga aaatactaca 420
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gagacttacc aggttaaacc ttgtcgtaat ctatgtggcc acagtatcgc accatatcgt 840
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ttcgaacaca ccatcttgtt gcatgctcac aaaaagggaag tcgtttcgaa aggtgatgac 1260
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Asp Glu Val Ala Arg Gln Leu Glu Arg Ser Ala Leu Glu Asp Lys Glu
 65 70 75 80

Arg Asp Glu Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Thr
 85 90 95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
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 145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175

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 180 185 190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
 210 215 220

Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
 245 250 255

Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270

Tyr Asp Thr Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285

Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300

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 305 310 315 320

Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Gln Tyr
 325 330 335

Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
 435 440 445
 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Leu
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 Val Ser Ala Val Gln Gln Glu Leu Asp Lys Glu Ser Gly Ala Leu Val
 50 55 60
 Asp Glu Val Ala Lys Gln Leu Glu Ser Gln Ala Leu Glu Glu Lys Glu
 65 70 75 80
 Arg Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Ala Asp Gly Ala Thr
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Lys Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160
 Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175

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 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Thr Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Pro Tyr
 325 330 335
 Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
 435 440 445
 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Leu
 450 455 460
 Arg Pro Thr Cys Lys Glu Val Val Ser Arg Gly Asp Asp Tyr
 465 470 475

<210> 14
 <211> 437
 <212> PRT
 <213> Yeast MetAP2

<400> 14

Met Thr Asp Ala Glu Ile Glu Asn Ser Pro Ala Ser Asp Leu Lys Glu
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 20 25 30
 Asp Glu Ser Asp Pro Val Glu Ser Lys Lys Lys Lys Asn Lys Lys Lys
 35 40 45
 Lys Lys Lys Lys Ser Asn Val Lys Lys Ile Glu Leu Leu Phe Pro Asp
 50 55 60
 Gly Lys Tyr Pro Glu Gly Ala Trp Met Asp Tyr His Gln Asp Phe Asn
 65 70 75 80
 Leu Gln Arg Thr Thr Asp Glu Glu Ser Arg Tyr Leu Lys Arg Asp Leu
 85 90 95
 Glu Arg Ala Glu His Trp Asn Asp Val Arg Lys Gly Ala Glu Ile His
 100 105 110
 Arg Arg Val Arg Arg Ala Ile Lys Asp Arg Ile Val Pro Gly Met Lys
 115 120 125
 Leu Met Asp Ile Ala Asp Met Ile Glu Asn Thr Thr Arg Lys Tyr Thr
 130 135 140
 Gly Ala Glu Asn Leu Leu Ala Met Glu Asp Pro Lys Ser Gln Gly Ile
 145 150 155 160
 Gly Phe Pro Thr Gly Leu Ser Leu Asn His Cys Ala Ala His Phe Thr
 165 170 175
 Pro Asn Ala Gly Asp Lys Thr Val Leu Lys Tyr Glu Asp Val Met Lys
 180 185 190
 Val Asp Tyr Gly Val Gln Val Asn Gly Asn Ile Ile Asp Ser Ala Phe
 195 200 205
 Thr Val Ser Phe Asp Pro Gln Tyr Asp Asn Leu Leu Ala Ala Val Lys
 210 215 220
 Asp Ala Thr Tyr Thr Gly Ile Lys Glu Ala Gly Ile Asp Val Arg Leu
 225 230 235 240
 Thr Asp Ile Gly Glu Ala Ile Gln Glu Val Met Glu Ser Tyr Glu Val
 245 250 255
 Glu Ile Asn Gly Glu Thr Tyr Gln Val Lys Pro Cys Arg Asn Leu Cys
 260 265 270
 Gly His Ser Ile Ala Pro Tyr Arg Ile His Gly Gly Lys Ser Val Pro
 275 280 285
 Ile Val Lys Asn Gly Asp Thr Thr Lys Met Glu Glu Gly Glu His Phe
 290 295 300
 Ala Ile Glu Thr Phe Gly Ser Thr Gly Arg Gly Tyr Val Thr Ala Gly
 305 310 315 320
 Gly Glu Val Ser His Tyr Ala Arg Ser Ala Glu Asp His Gln Val Met
 325 330 335
 Pro Thr Leu Asp Ser Ala Lys Asn Leu Leu Lys Thr Ile Asp Arg Asn
 340 345 350

Phe Gly Thr Leu Pro Phe Cys Arg Arg Tyr Leu Asp Arg Leu Gly Gln
 355 360 365
 Glu Lys Tyr Leu Phe Ala Leu Asn Asn Leu Val Arg His Gly Leu Val
 370 375 380
 Gln Asp Tyr Pro Pro Leu Asn Asp Ile Pro Gly Ser Tyr Thr Ala Gln
 385 390 395 400
 Phe Glu His Thr Ile Leu Leu His Ala His Lys Lys Glu Val Val Ser
 405 410 415
 Lys Gly Asp Asp Tyr Gly Lys Met Arg Phe Gln Met Ala Ser Ser Leu
 420 425 430
 Gly Ile Ile Leu Leu
 435

<210> 15
 <211> 71
 <212> PRT
 <213> Rat polylysine

<400> 15
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 Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val Asp Glu Val
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 Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu Lys Asp Asp
 35 40 45
 Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Ala Gly Lys Lys
 50 55 60
 Lys Lys Lys Lys Lys Lys Lys
 65 70

<210> 16
 <211> 480
 <212> PRT
 <213> Rat dnvMetAP2

<220>
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 <222> (219)
 <223> May be any naturally occurring amino acid

<220>
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 <222> (231)
 <223> May be any amino acid, except His

<220>
 <221> SITE
 <222> (251)
 <223> May be any naturally occurring amino acid

<220>
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 <222> (262)
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<220>
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 <222> (331)
 <223> May be any naturally occurring amino acid

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 <222> (338)..(339)
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 <223> May be any naturally occurring amino acid

<400> 16
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 Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Gly Lys Gly Ala
 35 40 45
 Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
 50 55 60
 Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
 65 70 75 80
 Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Ala
 85 90 95
 Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
 100 105 110
 Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
 115 120 125
 Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
 130 135 140
 Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
 145 150 155 160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
 165 170 175
 Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
 180 185 190
 Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
 195 200 205
 Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Xaa Pro Thr Gly Cys Ser
 210 215 220
 Leu Asn Asn Cys Ala Ala Xaa Tyr Thr Pro Asn Ala Gly Asp Thr Thr
 225 230 235 240
 Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Xaa Phe Gly Thr His Ile
 245 250 255
 Ser Gly Arg Ile Ile Xaa Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
 260 265 270
 Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
 275 280 285
 Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
 290 295 300
 Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
 305 310 315 320
 Gln Val Lys Pro Ile Arg Asn Xaa Asn Gly Xaa Ser Ile Gly Pro Tyr
 325 330 335
 Arg Xaa Xaa Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Xaa Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Xaa Pro Pro Xaa Cys
 435 440 445
 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Xaa His Thr Ile Leu Cys
 450 455 460
 Ala Gln Pro Val Lys Lys Leu Ser Ala Glu Glu Met Thr Ile Lys Thr
 465 470 475 480

<210> 17
 <211> 480

<212> PRT

<213> Rat MetAP2

<400> 17

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Met Ala Gly Val Glu Glu Ala Ser Ser Phe Gly Gly His Leu Asn Arg
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Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Thr Ser Ser Thr Ala Glu
      20              25              30

Glu Ala Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Gly Lys Gly Ala
      35              40              45

Val Ser Ala Gly Gln Gln Glu Leu Asp Lys Glu Ser Gly Thr Ser Val
      50              55              60

Asp Glu Val Ala Lys Gln Leu Glu Arg Gln Ala Leu Glu Glu Lys Glu
      65              70              75              80

Lys Asp Asp Asp Asp Glu Asp Gly Asp Gly Asp Gly Asp Gly Ala Ala
      85              90              95

Gly Lys Lys Lys Lys Lys Lys Lys Lys Arg Gly Pro Arg Val Gln
      100             105             110

Thr Asp Pro Pro Ser Val Pro Ile Cys Asp Leu Tyr Pro Asn Gly Val
      115             120             125

Phe Pro Lys Gly Gln Glu Cys Glu Tyr Pro Pro Thr Gln Asp Gly Arg
      130             135             140

Thr Ala Ala Trp Arg Thr Thr Ser Glu Glu Lys Lys Ala Leu Asp Gln
      145             150             155             160

Ala Ser Glu Glu Ile Trp Asn Asp Phe Arg Glu Ala Ala Glu Ala His
      165             170             175

Arg Gln Val Arg Lys Tyr Val Met Ser Trp Ile Lys Pro Gly Met Thr
      180             185             190

Met Ile Glu Ile Cys Glu Lys Leu Glu Asp Cys Ser Arg Lys Leu Ile
      195             200             205

Lys Glu Asn Gly Leu Asn Ala Gly Leu Ala Phe Pro Thr Gly Cys Ser
      210             215             220

Leu Asn Asn Cys Ala Ala His Tyr Thr Pro Asn Ala Gly Asp Thr Thr
      225             230             235             240

Val Leu Gln Tyr Asp Asp Ile Cys Lys Ile Asp Phe Gly Thr His Ile
      245             250             255

Ser Gly Arg Ile Ile Asp Cys Ala Phe Thr Val Thr Phe Asn Pro Lys
      260             265             270

Tyr Asp Ile Leu Leu Lys Ala Val Lys Asp Ala Thr Asn Thr Gly Ile
      275             280             285

Lys Cys Ala Gly Ile Asp Val Arg Leu Cys Asp Val Gly Glu Ala Ile
      290             295             300

Gln Glu Val Met Glu Ser Tyr Glu Val Glu Ile Asp Gly Lys Thr Tyr
      305             310             315             320

Gln Val Lys Pro Ile Arg Asn Leu Asn Gly His Ser Ile Gly Pro Tyr
      325             330             335

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Arg Ile His Ala Gly Lys Thr Val Pro Ile Val Lys Gly Gly Glu Ala
 340 345 350
 Thr Arg Met Glu Glu Gly Glu Val Tyr Ala Ile Glu Thr Phe Gly Ser
 355 360 365
 Thr Gly Lys Gly Val Val His Asp Asp Met Glu Cys Ser His Tyr Met
 370 375 380
 Lys Asn Phe Asp Val Gly His Val Pro Ile Arg Leu Pro Arg Thr Lys
 385 390 395 400
 His Leu Leu Asn Val Ile Asn Glu Asn Phe Gly Thr Leu Ala Phe Cys
 405 410 415
 Arg Arg Trp Leu Asp Arg Leu Gly Glu Ser Lys Tyr Leu Met Ala Leu
 420 425 430
 Lys Asn Leu Cys Asp Leu Gly Ile Val Asp Pro Tyr Pro Pro Leu Cys
 435 440 445
 Asp Ile Lys Gly Ser Tyr Thr Ala Gln Phe Glu His Thr Ile Leu Cys
 450 455 460
 Ala Gln Pro Val Lys Lys Leu Ser Ala Glu Glu Met Thr Ile Lys Thr
 465 470 475 480

<210> 18
 <211> 1944
 <212> DNA
 <213> Rat MetAP2 variant

<220>
 <221> misc_feature
 <222> (779)
 <223> Any nucleotide

<400> 18
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 gccacctgaa tcgcgacctg gatccagacg acagggaaga gggaacctcc agcacggccg 180
 aggaagccgc caagaagaaa agacggaaga agaagaaggg caaaggggct gtgtcagcag 240
 ggcaacaaga acttgataaa gaatcgggaa cctcagtggg cgaagtagca aaacagttgg 300
 agagacaagc actggaggag aaagagaaa atgatgacga tgaagatgga gatggtgatg 360
 gtgatggtgc agctgggaag aagaagaaa agaagaagaa gaagagagga ccaagagttc 420
 aaacagaccc tccctcagtt ccaatatgtg acctgtatcc taatggtgta tttcccaaag 480
 gacaagagtg tgaataccca cccacccaag atgggcggac agctgcttgga agaaccacaa 540
 gtgaagagaa aaaggcgcta gaccaggcta gtgaggagat ttggaacgac ttccgagaag 600
 ctgccgaagc acaccggcaa gttaggaaat acgtcatgag ctggatcaag cctgggatga 660
 caatgataga aatatgtgag aagtgggaag actgttcccg aaagctcata aaggagaatg 720
 ggttaaatgc aggctggcc tttccactg ggtgttctct caacaactgt gctgcagcnt 780
 acactcccaa tgctgggtgac acgacagtct tacagtacga cgacatctgt aagatcgact 840
 ttggaacgca tataagtggg agaataattg attgtgcttt tactgttact ttaaatccca 900
 aatatgacat attattaaaa gctgtaaaag atgccaccaa tactggaata aagtgtgagg 960
 ggattgacgt ccgtctctgt gatgtcggcg aggccattca agaagttatg gagtctatg 1020
 aagtggaaat agatgggaag acctaccaag tgaaacccat acgtaactta aatggacatt 1080
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 gcgtggttca tgacgatatg gaatgttcac actacatgaa aaattttgat gtgggacacg 1260
 tgccaataag gcttccaaga acaaaacact tgttgaatgt catcaatgaa aactttggta 1320
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tgaagaacct gtgtgacttg ggcattgtag atccatatcc accactctgt gacattaaag 1440
gatcatacac agcacagttt gaacatacca tactctgcgc ccaacctgta aagaagttgt 1500
cagcagagga gatgactatt aaaacttagt ccaaagccaa ctcaacgtct ttattttcta 1560
agctttgttg gaacacatta taccacaagt aatttgcaac atgtctgttt taacagtggg 1620
cctgtgtaat gccgttatcc atgtttaaag gagtttgatc aaagccaaac tgtctacatg 1680
taattaacca aggaaaaggc tttcaagact ttactgttaa ctgtttctcc cgtctaggaa 1740
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tgcttttttg atatttatat tgccatattc ttacttggat gctttgaatg actacataca 1860
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<210> 19

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
transit peptide

<400> 19

Gly Arg Lys Lys Arg Arg Gln Arg

1

5

<210> 20

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
oligonucleotide

<400> 20

gcgcaagctt atgattgaat tactgtttcc agatggaaag

40

<210> 21

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
oligonucleotide

<400> 21

gcgccctcgag tcagtagtca tcacctttcg aaacg

35

<210> 22

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
peptide

<400> 22

Cys Lys Glu Val Val Ser Lys Gly Asp Asp Tyr

1

5

10

<210> 23

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic peptide

<400> 23

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<210> 24

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic peptide

<400> 24

Met Gly Met Met
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<210> 25

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 25

cacactcgac cgcgatgtac tactactact actactacta ctactacggg ccagatatac 60
gcg 63

<210> 26

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic oligonucleotide

<400> 26

cacagaattc cccgcatccc cagcatgcct gctattg

37